

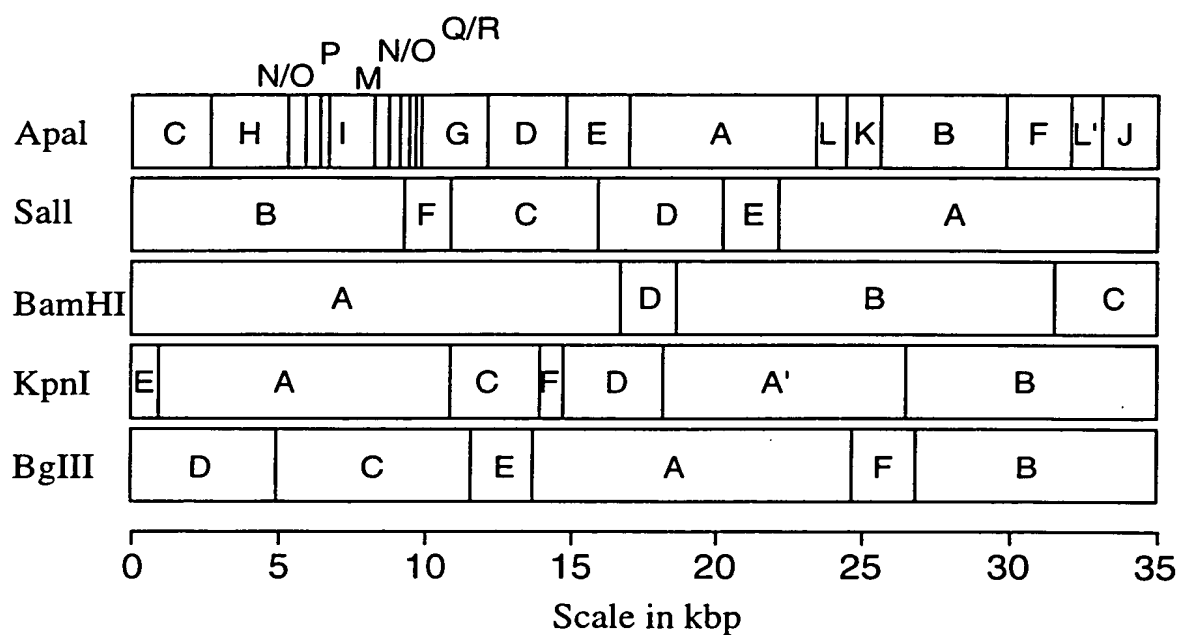
APPROVED	C.E. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

ART 34
PCT/AU98/00648
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Fig 1.

Restriction enzyme maps of the PAV3 genome



005550" 2158460

APPROVED	O.G. FIG.	
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Fig 2.

Total sequence of the PAV Major Late Promoter cassette including the added nucleotides 5' (upstream) of the USF.

Nucleotide base count: 76 A 143 C 187 G 96 T Total 502 bp

```

1  GGTGCCGCGG TCGTCGGCGT AGAGGATGAG GGCCCGAGTCG GAGATGAAGG CACGCGCCCA
61  GCGGAGGACG AAGCTGGCGA CCTCCGAGGG GTAGCGGTCG TTGGGCACTA ATGGCGAGGC
121 CTGCTCGAGC GTGTGGAGAC AGAGTCCTC GTCGTCCGCG TCCAGGAAGT GGATTGGTCG
181 CCAGTGGTAG TCCACGTGAC CGGCTTCCGG GTCGGGGGGT ATAAAGGCGCGGCCGGGG
241 TCGGTGGCCG TCAGTTGCTT CGCAGGCCTC GTCACCGGAG TCCGCGTCTC CGGCGTCTCG
301 CGCTGCGGCT GCATCTGTGG TCCCGAGTC TTCAGGTCCT TGTGAGGAG GTACTCCTGA
361 TCGCTGTCCC AGTACTTGGC GTGTGGGAAG CCGTCCTGAT CGCGATCCTC CTGCTGTTGC
421 AGCGCTTCGG CAAACACGGC CACCTGCTCT TCGGACCCGG CGAAGCGTTC GACGAAGGCG
481 TCTAGCCAGC AACAGTCGCA AG
  
```

The Upstream Stimulatory Factor (USF) and TATA motif are in **bold**. The complete leader sequence is italicised with the cap site and splice sites between the individual leaders indicated by double underlining or single underlining respectively.

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Fig 3.

Individual sequences of the Promoter cassette components:

I. The 5' (upstream) sequence included in the long cassette.

```

1      GGTGCCCGCG TCGTCGGCGT AGAGGATGAG GGCCAGTCG GAGATGAAGG CACGCGCCCA
61     GGCGAGGACG AAGCTGGCGA CCTGCGAGGG GTAGCGGTCG TTGGGCACTA ATGGCGAGGC
121    CTGCTCGAGC GTGTGGAGAC AGAGGTCCTC GTCGTCCGCG TCCAGGAAGT GGATTGGTCG
181    CCAGTGGTAG

```

II. Sequence including the USF, TATA motif and sequence to the cap site.

```

1      CCACGTGACC GGCTTGCGGG TCGGGGGGTA TAAAAGGCGC GGGCCGGGGT GCGTGGCCGT
61     C

```

III. First leader sequence.

```

1      AGTTGCTTCG CAGGCCTCGT CACCGGAGTC CGCGTCTCCG GCGTCTCGCG CTGCGGCTGC
61     ATCTGTGGTC CCGGAGTCTT CAG

```

IV. Second leader sequence.

```

1      GTCCTTGTTG AGGAGGTACT CCTGATCGCT GTCCAGTAC TTGGCGTGTG GGAAGCCGTC
61     CTGATCG

```

V. Third leader sequence.

```

1      CGATCCTCCT GCTGTTGCAG CGCTTCGGCA AACACGCGCA CCTGCTCTTC GGACCCGGCG
61     AAGCGTTCGA CGAAGGCGTC TAGCCAGCAA CAGTCGCAAG

```

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Sequence of the right hand end of the PAV genome this area being a proposed site for insertion of expression cassettes.

Nucleotide base count 183 A 255 C 306 G 204 T Total 948 bases

1 CATCATCAAT AATATACCGC ACACCTTTTAT TGCCCCCTTTT GTGGCGGTGGT GATTGGCGGA
61 GAGGGTTGGG GCGCGCGGGC GGTGATTGGT GGAGAGGGGT GTGACGTAGC GTGGGAACGT
121 GACGTCGCGT GGGAAAATAA CGTGCGGTGG GAACGGTCAA AGTCCGAGG GCGGGGTCAA
181 AGTCCGCAGT CCGCGGGCGG AGCCGGCTGG CCGGAATTCC EcorI SmaI TGGGCGGGTA
241 ATCGTTAAGC HpaI EcorI TCGGACGATG TGGTACTGAT TAACCGACCG
301 CAGGCGGTGC CACATCCGCT GTGGGTATAT CACCGGCGCT CGCGGTGTTC GCTCACACTC
361 GTCTCGGCGC TGTACACAG AGAGACACTG AGAGCGAGAC GAGGAGAAAC CGAAAGCGGG
421 GCAGGAGGAG TCACCGGGCC ATCTTCCCAT CAGAGCCCTC TCATGGCCCA CGACCGACTG
481 CTGCTGGCCG CCGTGGCTGA CTGTTGCTCG CCGTGTCTTA TCTGTACTTC GCCTACCTCG
541 CGTGGCAGGA TCGGGACACT CTTCACACTC AGGAGGCCCG CTCTCCTCGC TTCTTCATCG
601 GGTCCAACCA CCAGCCCTGG TGCCCGGATT TTGATTGGCA GGAGCAGGAC GAGCACACTC
661 ACTAGACGTT TAGAAAAAG ACACACATTG GAACCTCATAT ATGCTGCGG GACCGCATCA
721 GCAGCCCGGT CTGCTGTTGG CTGCGGGTGA GAGGCTCCG StuI AGAACCGCAT
781 TCATCTGCGC CACGTCCCGA CATATGGTGC TGACCTCAGA ACAGCCCGAC GTGATCCTTT
841 TAATGTGCTA GTCTACGTGC CCACTGGGTT TGCTGTGTTT SacII AGCGAGATT
901 TCAGAGGAGG GATCTGGTCC GTTCCAGAC CTGCTGCTTC CGGCATCA

The Inverted Terminal Repeat (ITR) is shown in bold. Enzyme sites of interest are underlined with the enzyme name below. Putative TATA for E4 region is also shown.

Fig 4.

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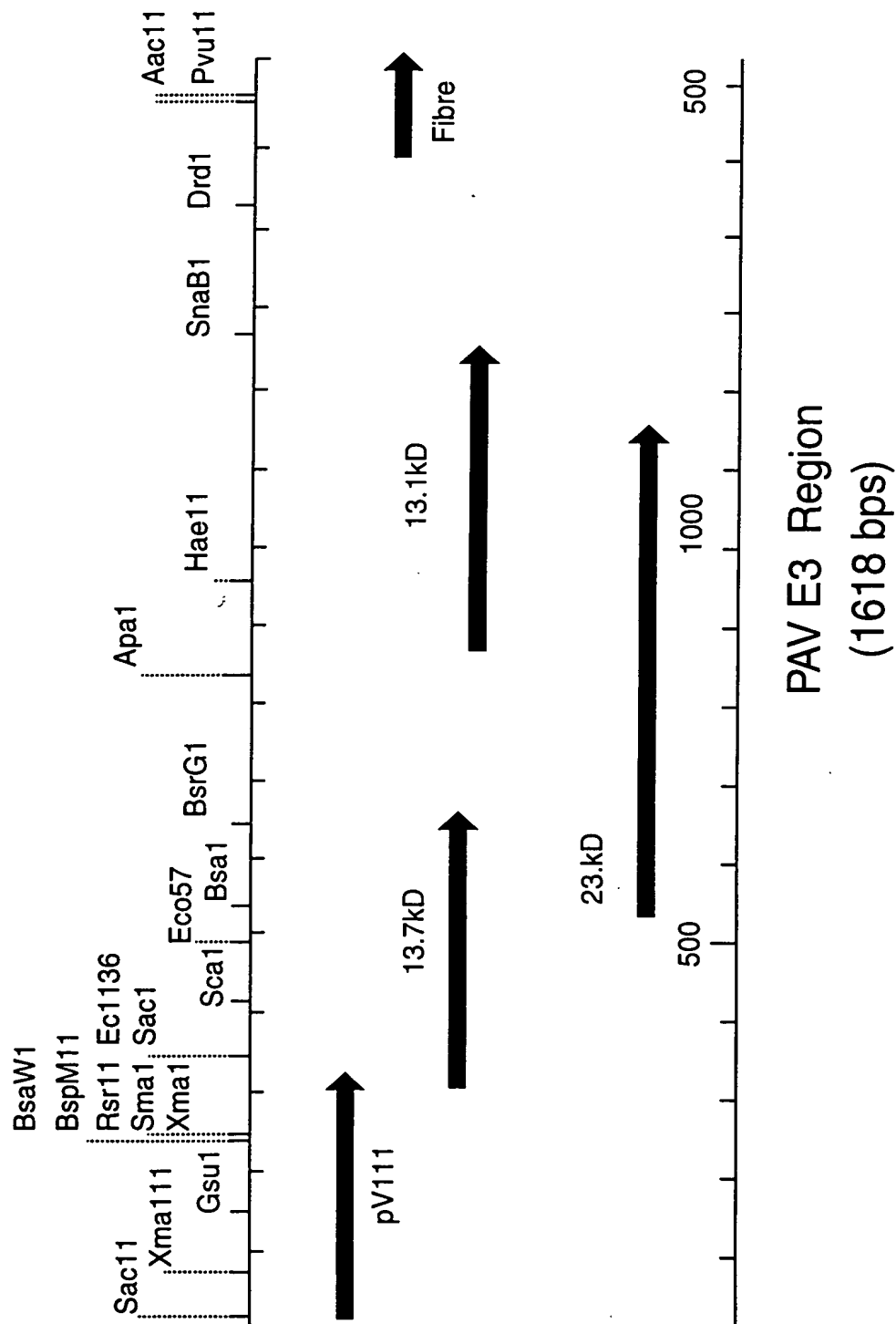
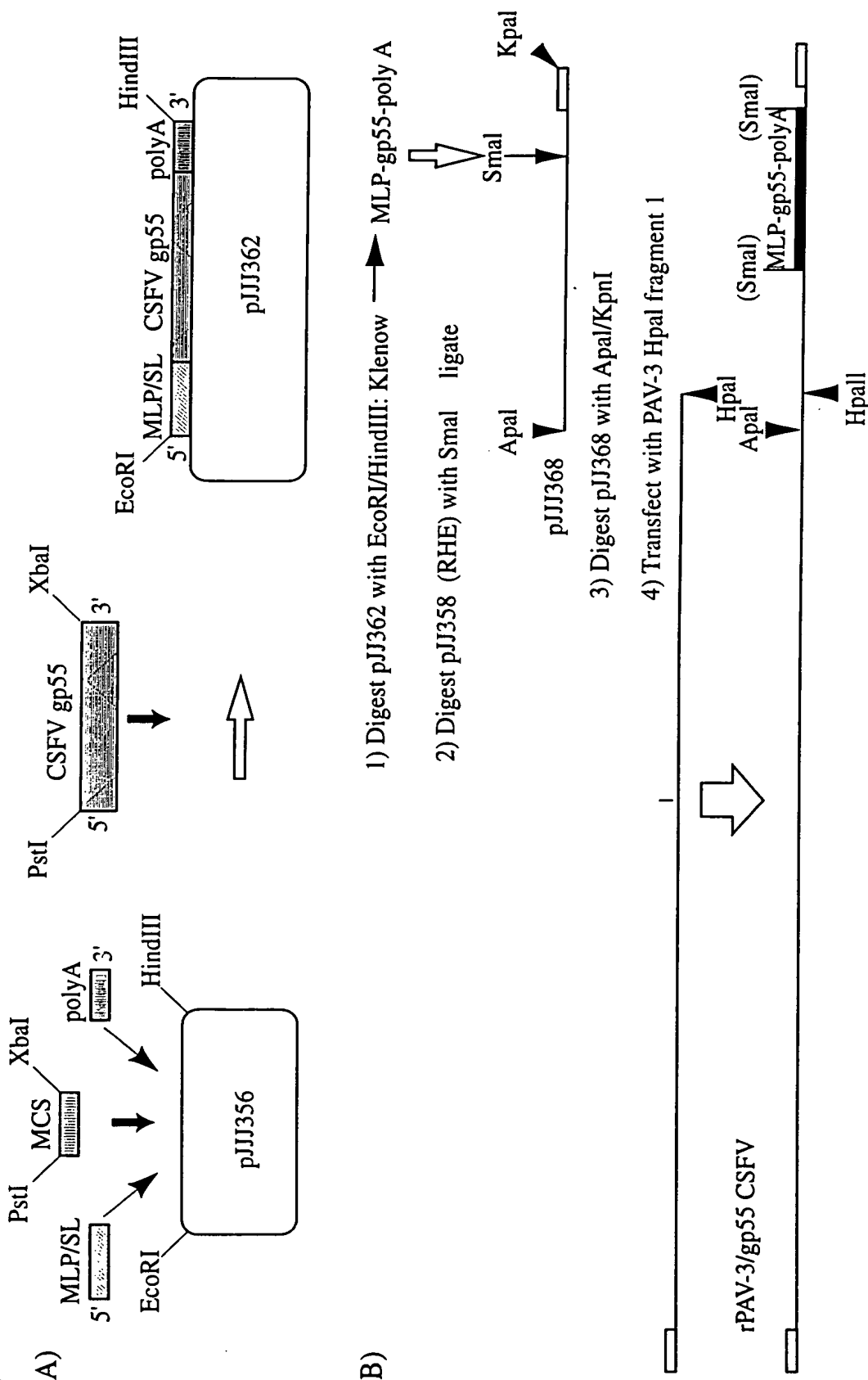


Fig 5.

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Fig 6.



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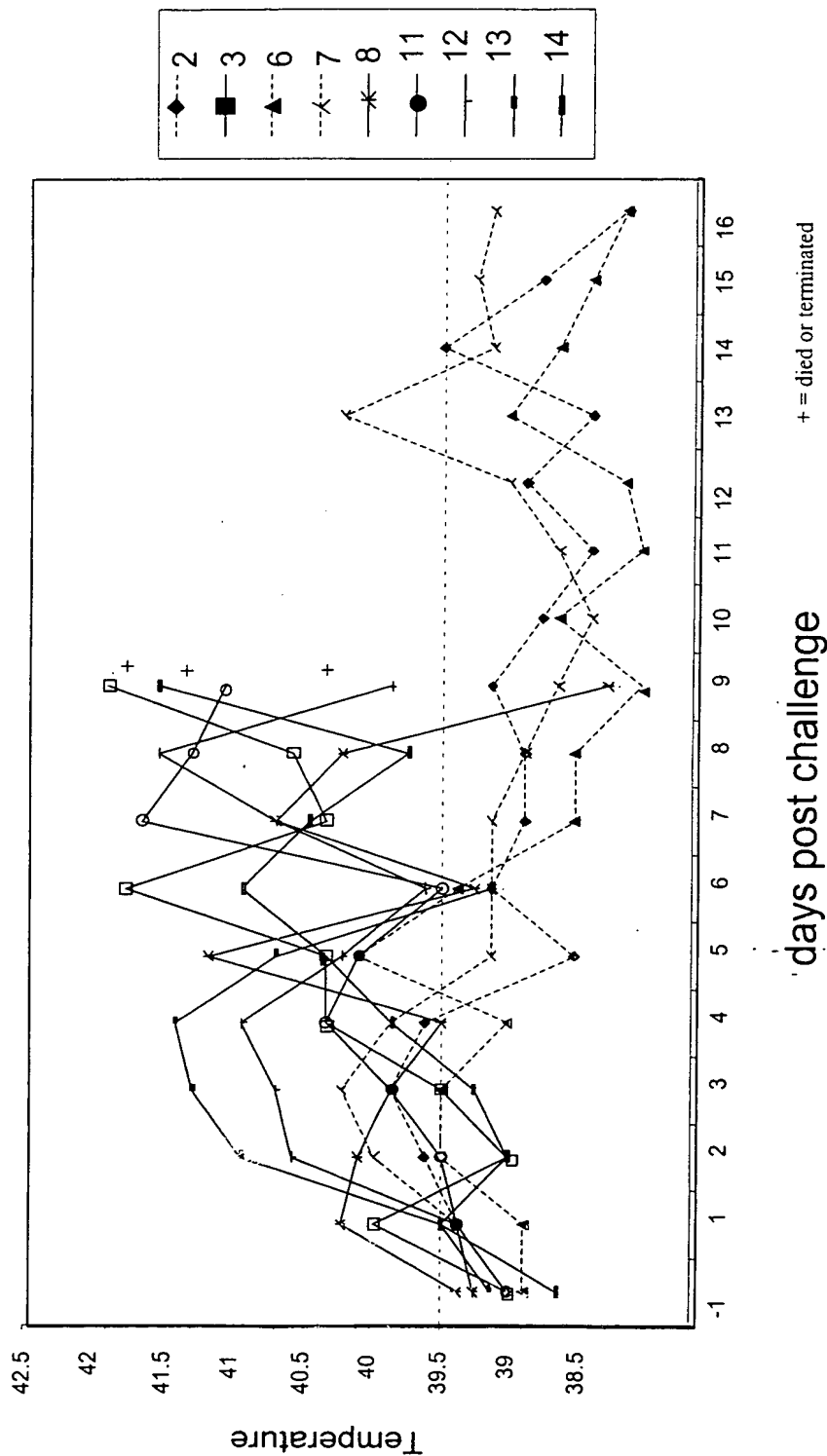


FIGURE 7

APPROVED	J.C. FIG.	
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FIGURE 8

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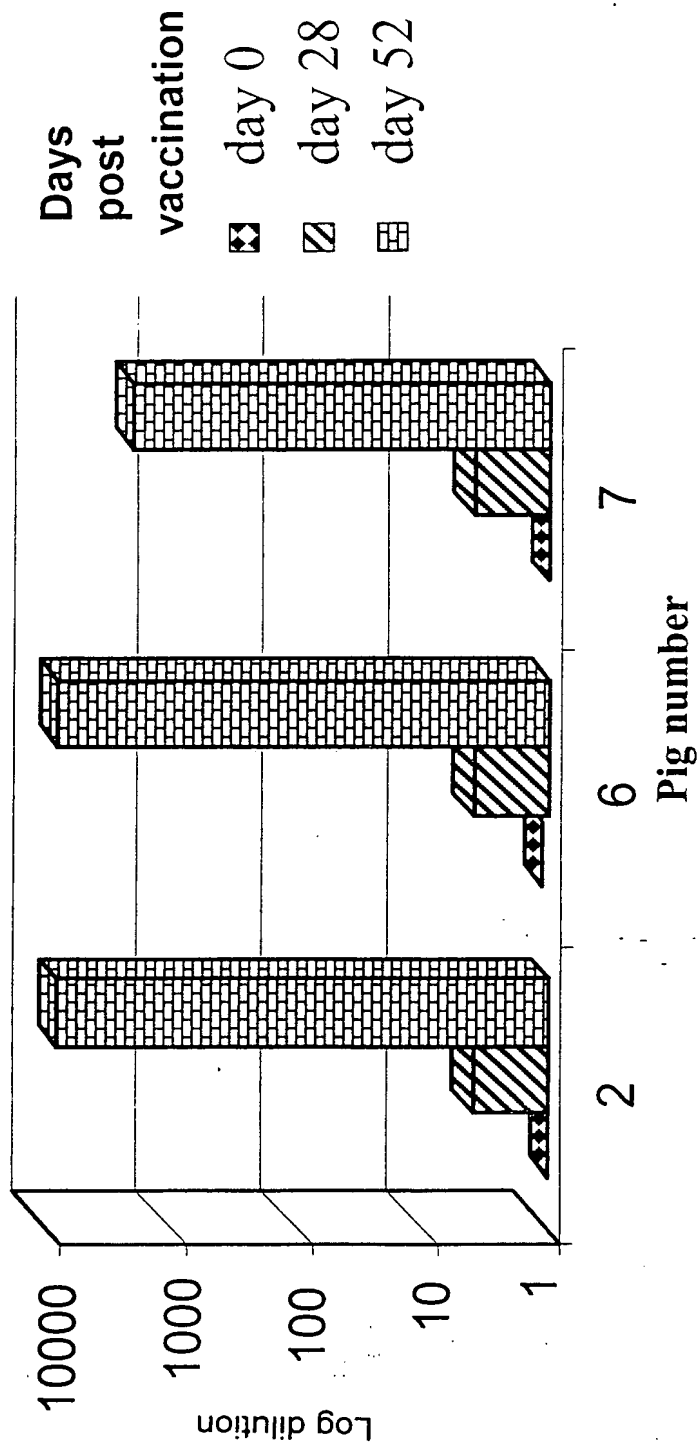
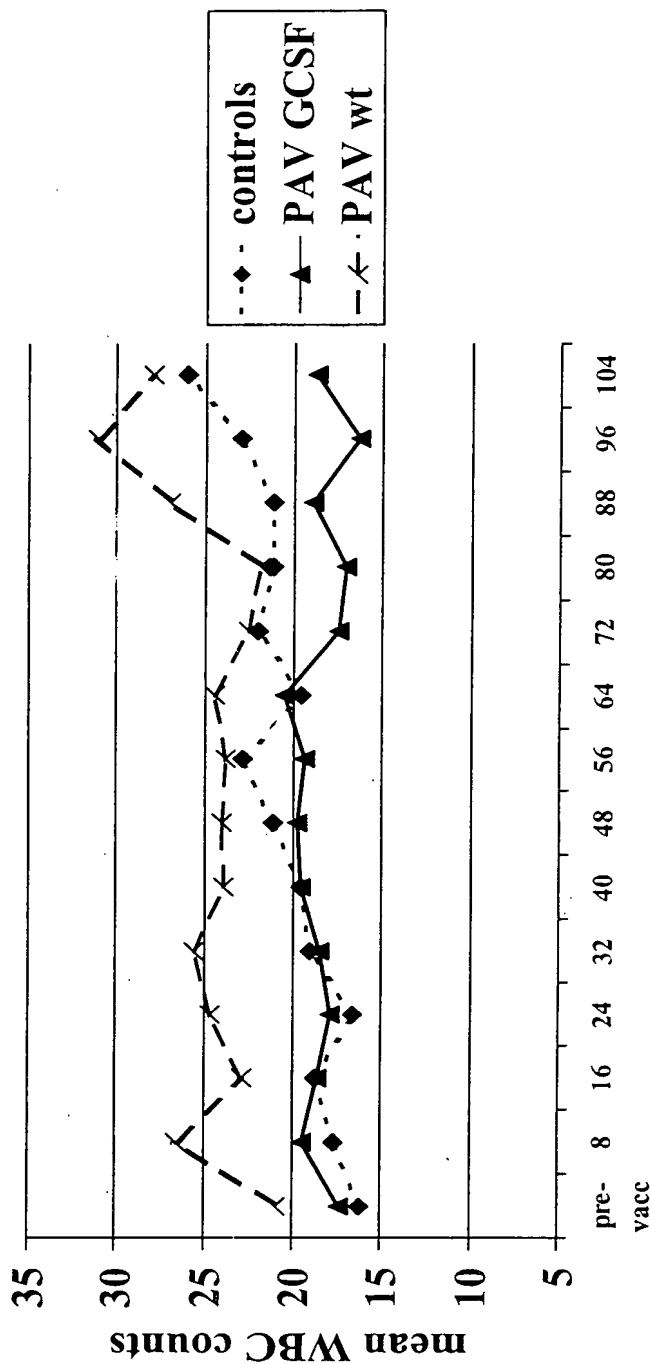


FIGURE 9



Hours post vaccination

FIGURE 10

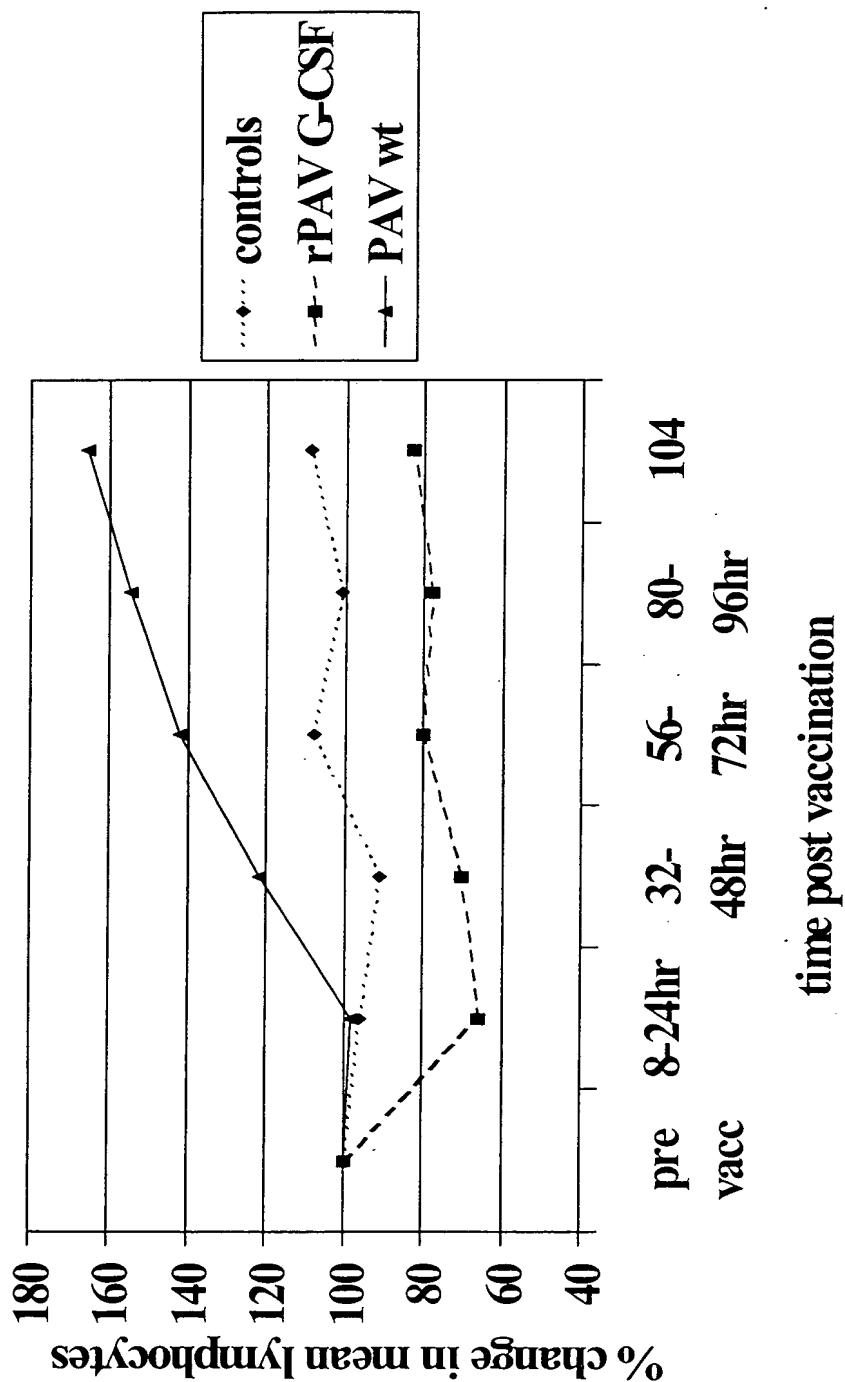


FIGURE 11

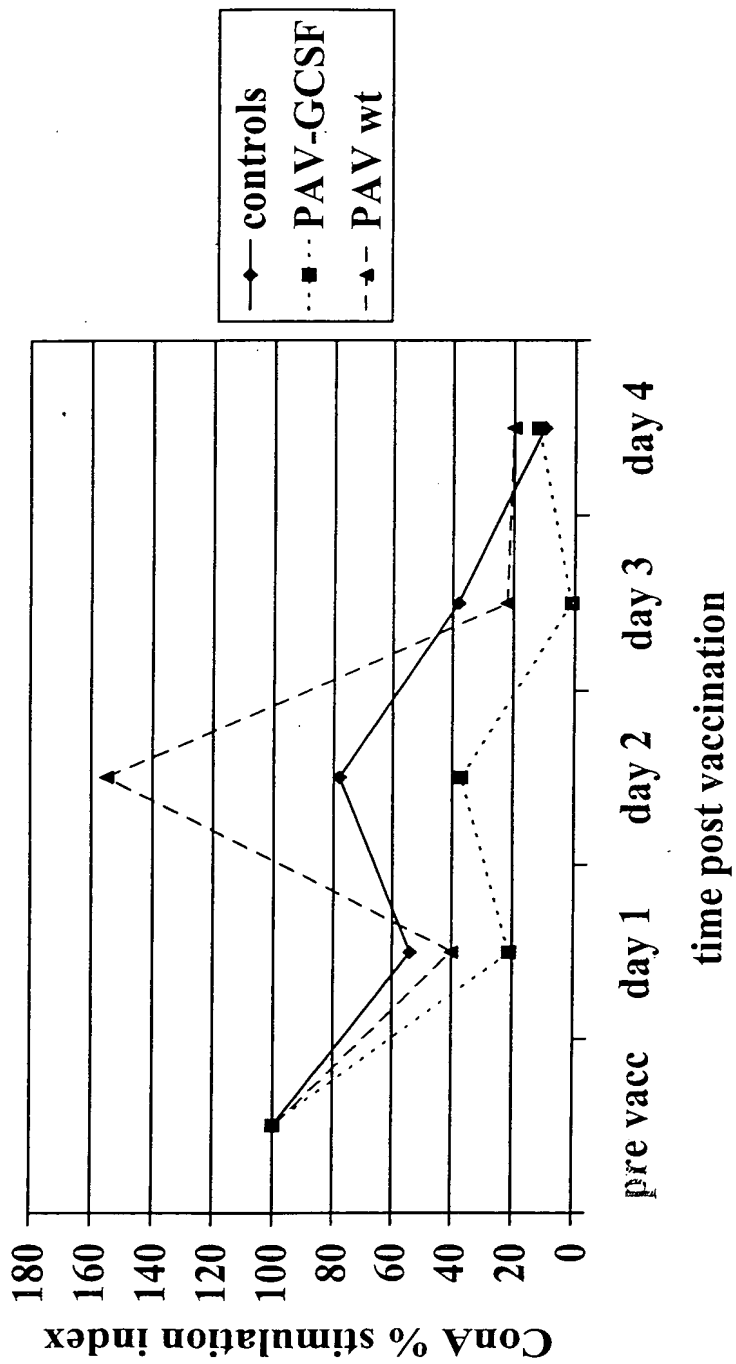


FIGURE 12

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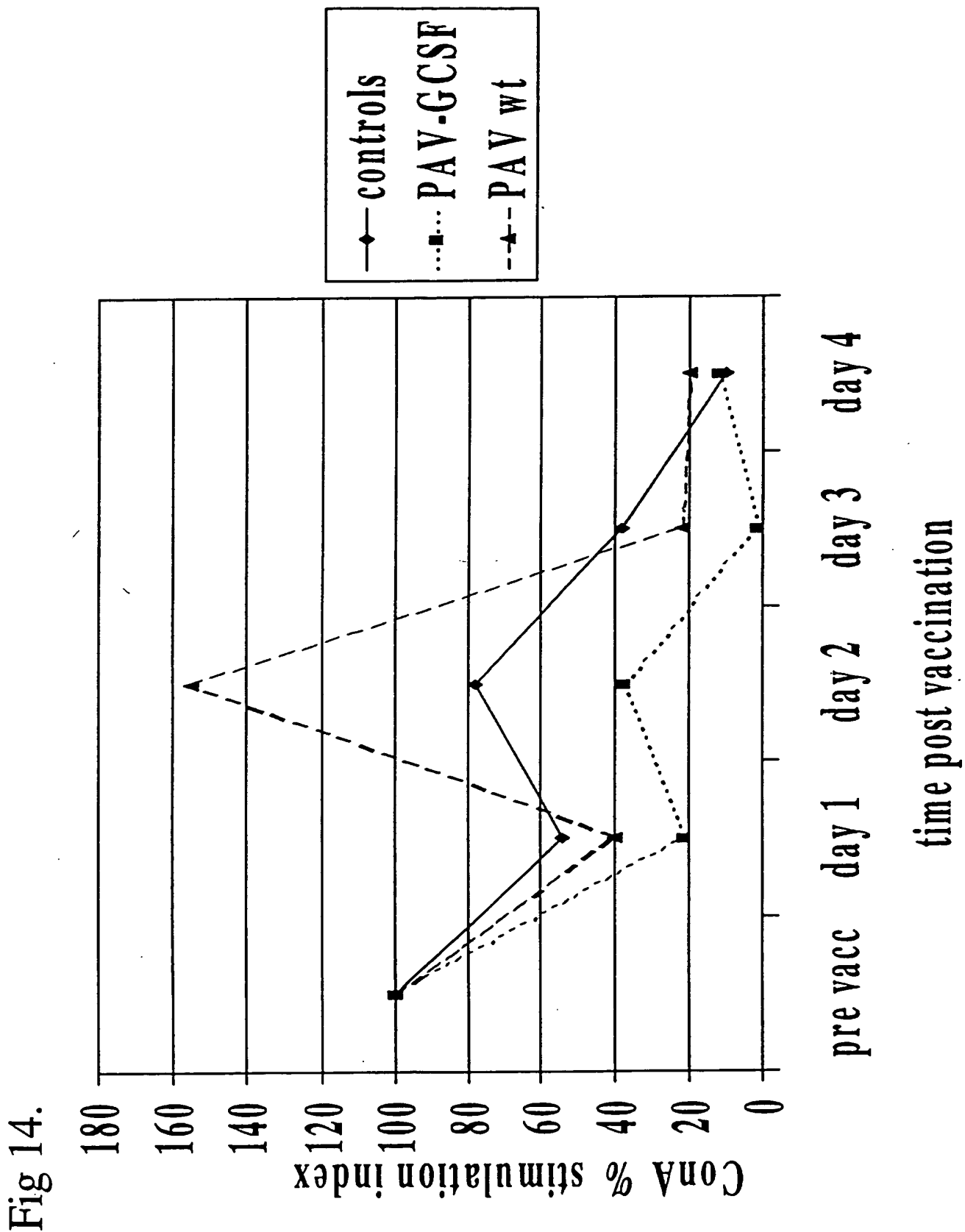


Fig 15.

